Supporting Material

Table S1. The sample characteristics of relative intensities of cleavage of central phosphodiester bond in 256 tetranucleotides.

	N	$\bar{R}$	S	$S_{\bar{R}}$	The 95% confidence limits	
					Lower limit	Upper limit
AAAA	232	0.894	0.132	0.009	0.877	0.911
AAAC	151	0.883	0.139	0.011	0.860	0.905
AAAG	93	0.915	0.107	0.013	0.893	0.937
AAAT	96	0.951	0.142	0.013	0.922	0.980
CAAA	114	0.921	0.169	0.012	0.890	0.952
CAAC	80	0.877	0.118	0.015	0.851	0.904
CAAG	77	0.938	0.142	0.015	0.906	0.970
CAAT	77	0.935	0.126	0.015	0.907	0.964
GAAA	119	0.921	0.113	0.012	0.900	0.941
GAAC	49	0.887	0.117	0.019	0.853	0.921
GAAG	88	0.936	0.113	0.014	0.912	0.960
GAAT	132	0.917	0.127	0.011	0.895	0.939
TAAA	108	0.952	0.125	0.013	0.928	0.976
TAAC	73	0.916	0.097	0.015	0.894	0.939
TAAG	55	0.997	0.155	0.018	0.955	1.039
TAAT	95	0.929	0.124	0.013	0.903	0.954
AACA	96	0.938	0.112	0.011	0.915	0.960
AACC	77	0.881	0.131	0.015	0.852	0.911
AACG	100	0.923	0.128	0.013	0.897	0.948
AACT	78	0.919	0.127	0.014	0.890	0.947
CACA	58	0.943	0.151	0.020	0.903	0.982
CACC	85	0.820	0.130	0.014	0.792	0.848
CACG	46	0.871	0.174	0.026	0.819	0.922
CACT	73	0.900	0.116	0.014	0.873	0.927
GACA	59	0.935	0.166	0.022	0.891	0.978
GACC	34	0.921	0.117	0.020	0.880	0.962
GACG	83	0.913	0.156	0.017	0.879	0.947
GACT	61	0.914	0.129	0.016	0.889	0.952

TACA	38	0.986	0.094	0.015	0.937	1.013
TACC	79	0.887	0.113	0.013	0.862	0.913
TACG	71	0.921	0.101	0.012	0.897	0.945
TACT	43	0.973	0.114	0.017	0.938	1.008
AAGA	70	0.905	0.098	0.012	0.881	0.928
AAGC	91	0.845	0.142	0.015	0.815	0.874
AAGG	72	0.924	0.133	0.016	0.893	0.955
AAGT	79	0.899	0.108	0.012	0.875	0.923
CAGA	81	0.935	0.146	0.016	0.899	0.964
CAGC	100	0.846	0.136	0.014	0.819	0.873
CAGG	82	0.932	0.128	0.014	0.904	0.960
CAGT	92	0.897	0.137	0.014	0.868	0.925
GAGA	50	0.880	0.118	0.017	0.846	0.914
GAGC	59	0.889	0.109	0.014	0.861	0.917
GAGG	48	0.914	0.117	0.017	0.867	0.935
GAGT	50	0.874	0.107	0.015	0.844	0.905
TAGA	41	0.935	0.082	0.013	0.909	0.961
TAGC	50	0.907	0.114	0.016	0.874	0.939
TAGG	40	0.886	0.145	0.023	0.840	0.933
TAGT	26	0.975	0.197	0.039	0.896	1.055
AATA	110	0.925	0.121	0.012	0.902	0.948
AATC	65	0.913	0.117	0.014	0.884	0.942
AATG	98	0.913	0.127	0.013	0.887	0.938
AATT	129	0.875	0.115	0.010	0.855	0.895
CATA	75	0.910	0.137	0.016	0.878	0.941
CATC	67	0.801	0.189	0.023	0.755	0.847
CATG	70	0.879	0.103	0.012	0.855	0.903
CATT	88	0.863	0.108	0.011	0.840	0.886
GATA	91	0.907	0.083	0.009	0.890	0.924
GATC	92	0.950	0.120	0.012	0.925	0.975
GATG	77	0.929	0.113	0.013	0.903	0.954
GATT	76	0.913	0.107	0.012	0.888	0.937
TATA	67	0.913	0.129	0.016	0.881	0.945
TATC	89	0.858	0.114	0.012	0.834	0.882
TATG	69	0.946	0.106	0.013	0.920	0.971
TATT	115	0.914	0.132	0.012	0.889	0.938
ACAA	57	1.103	0.176	0.023	1.056	1.149
ACAC	53	1.108	0.177	0.024	1.059	1.156
ACAG	86	1.183	0.213	0.023	1.137	1.228
ACAT	67	1.116	0.181	0.022	1.072	1.160
CCAA	73	1.025	0.178	0.021	0.984	1.067

CCAC	45	0.989	0.149	0.022	0.944	1.033
CCAG	96	1.190	0.213	0.022	1.147	1.233
CCAT	81	1.073	0.168	0.019	1.035	1.110
GCAA	126	1.223	0.204	0.018	1.187	1.259
GCAC	71	1.174	0.215	0.026	1.123	1.225
GCAG	89	1.356	0.263	0.028	1.301	1.412
GCAT	73	1.186	0.203	0.024	1.139	1.234
TCAA	93	1.127	0.171	0.018	1.092	1.162
TCAC	94	1.112	0.144	0.015	1.082	1.141
TCAG	84	1.231	0.266	0.029	1.173	1.288
TCAT	80	1.129	0.200	0.022	1.085	1.174
ACCA	78	0.975	0.112	0.013	0.949	1.000
ACCC	72	0.986	0.147	0.017	0.952	1.021
ACCG	79	1.064	0.143	0.016	1.032	1.096
ACCT	45	1.012	0.101	0.015	0.981	1.042
CCCA	45	0.930	0.093	0.014	0.902	0.958
CCCC	107	0.912	0.115	0.011	0.890	0.934
CCCG	103	0.992	0.147	0.014	0.964	1.021
CCCT	59	0.941	0.138	0.018	0.904	0.977
GCCA	118	1.080	0.153	0.014	1.052	1.108
GCCC	50	1.085	0.223	0.032	1.022	1.148
GCCG	48	1.130	0.130	0.019	1.092	1.168
GCCT	61	1.086	0.150	0.019	1.048	1.125
TCCA	53	0.999	0.127	0.018	0.964	1.035
TCCC	88	0.943	0.113	0.012	0.919	0.967
TCCG	70	1.035	0.149	0.018	0.999	1.070
TCCT	70	0.966	0.130	0.016	0.935	0.997
ACGA	86	1.537	0.331	0.036	1.466	1.608
ACGC	96	1.362	0.309	0.032	1.299	1.424
ACGG	61	1.483	0.283	0.036	1.410	1.555
ACGT	53	1.381	0.369	0.051	1.279	1.482
CCGA	63	1.432	0.309	0.039	1.354	1.510
CCGC	91	1.257	0.220	0.023	1.211	1.303
CCGG	91	1.417	0.311	0.033	1.352	1.482
CCGT	55	1.328	0.246	0.033	1.262	1.395
GCGA	100	1.783	0.577	0.058	1.668	1.897
GCGC	87	1.462	0.358	0.038	1.385	1.538
GCGG	102	1.549	0.334	0.033	1.483	1.614
GCGT	72	1.427	0.324	0.038	1.351	1.503
TCGA	47	1.543	0.371	0.054	1.434	1.652
TCGC	104	1.300	0.282	0.028	1.245	1.355
TCGG	65	1.543	0.265	0.033	1.477	1.608

TCGT	58	1.263	0.227	0.030	1.203	1.323
ACTA	44	1.160	0.210	0.032	1.096	1.224
ACTC	74	1.064	0.134	0.016	1.033	1.095
ACTG	58	1.157	0.243	0.032	1.093	1.221
ACTT	69	1.060	0.158	0.019	1.022	1.097
CCTA	23	1.031	0.145	0.030	0.968	1.093
CCTC	73	0.980	0.128	0.015	0.950	1.010
CCTG	73	1.118	0.157	0.018	1.082	1.155
CCTT	67	1.029	0.120	0.015	0.999	1.058
GCTA	40	1.227	0.166	0.026	1.173	1.280
GCTC	90	1.256	0.227	0.024	1.208	1.303
GCTG	112	1.303	0.216	0.020	1.262	1.343
GCTT	88	1.210	0.225	0.024	1.162	1.257
TCTA	31	1.098	0.068	0.012	1.073	1.123
TCTC	56	0.992	0.131	0.018	0.957	1.027
TCTG	101	1.149	0.195	0.019	1.111	1.188
TCTT	81	1.042	0.188	0.021	1.000	1.083
AGAA	96	0.986	0.117	0.012	0.962	1.010
AGAC	30	0.979	0.137	0.025	0.928	1.031
AGAG	48	0.956	0.144	0.021	0.914	0.998
AGAT	69	1.003	0.127	0.015	0.972	1.033
CGAA	100	0.982	0.205	0.020	0.941	1.023
CGAC	84	0.914	0.150	0.016	0.881	0.946
CGAG	52	0.962	0.102	0.014	0.933	0.990
CGAT	61	1.008	0.223	0.029	0.951	1.066
GGAA	102	0.968	0.123	0.012	0.943	0.992
GGAC	26	0.979	0.136	0.027	0.924	1.034
GGAG	31	0.898	0.175	0.031	0.834	0.962
GGAT	98	0.998	0.155	0.016	0.967	1.029
TGAA	88	0.936	0.124	0.013	0.910	0.962
TGAC	87	0.964	0.117	0.013	0.939	0.989
TGAG	77	0.997	0.106	0.012	0.973	1.021
TGAT	105	0.987	0.123	0.012	0.963	1.011
AGCA	95	0.975	0.136	0.014	0.947	1.003
AGCC	46	0.922	0.136	0.020	0.881	0.962
AGCG	73	1.029	0.136	0.016	0.997	1.060
AGCT	84	0.974	0.145	0.016	0.942	1.005
CGCA	99	0.969	0.115	0.012	0.946	0.992
CGCC	106	0.886	0.173	0.017	0.853	0.919
CGCG	92	0.974	0.171	0.018	0.938	1.009
CGCT	82	0.929	0.146	0.016	0.897	0.961

GGCA	75	0.913	0.128	0.015	0.884	0.943
GGCC	68	0.868	0.121	0.015	0.839	0.897
GGCG	104	0.967	0.169	0.017	0.934	1.000
GGCT	58	0.982	0.144	0.019	0.944	1.020
TGCA	88	0.931	0.134	0.014	0.903	0.960
TGCC	55	0.958	0.143	0.019	0.919	0.996
TGCG	94	1.016	0.174	0.018	0.981	1.052
TGCT	87	1.008	0.155	0.017	0.975	1.041
AGGA	37	0.943	0.100	0.016	0.910	0.977
AGGC	70	0.905	0.150	0.018	0.869	0.941
AGGG	89	0.989	0.153	0.016	0.957	1.021
AGGT	46	0.921	0.155	0.023	0.875	0.967
CGGA	89	0.962	0.112	0.012	0.938	0.985
CGGC	69	0.831	0.133	0.016	0.799	0.863
CGGG	63	0.902	0.159	0.020	0.862	0.942
CGGT	100	0.925	0.148	0.015	0.895	0.954
GGGA	76	0.939	0.165	0.019	0.901	0.976
GGGC	71	0.881	0.155	0.018	0.844	0.917
GGGG	84	0.958	0.160	0.018	0.923	0.993
GGGT	71	0.948	0.121	0.014	0.920	0.977
TGGA	54	0.944	0.152	0.021	0.902	0.985
TGGC	93	0.859	0.142	0.015	0.830	0.888
TGGG	65	0.885	0.134	0.017	0.852	0.919
TGGT	93	0.922	0.130	0.013	0.895	0.949
AGTA	36	0.972	0.083	0.014	0.944	1.001
AGTC	38	0.909	0.170	0.028	0.853	0.965
AGTG	59	0.972	0.099	0.013	0.946	0.998
AGTT	112	0.965	0.125	0.012	0.941	0.988
CGTA	60	0.987	0.081	0.010	0.966	1.008
CGTC	57	0.908	0.165	0.022	0.864	0.952
CGTG	32	0.981	0.178	0.031	0.917	1.045
CGTT	91	0.940	0.138	0.014	0.911	0.968
GGTA	87	0.959	0.123	0.013	0.933	0.985
GGTC	30	0.904	0.139	0.025	0.852	0.956
GGTG	88	0.966	0.134	0.014	0.938	0.995
GGTT	103	0.938	0.118	0.012	0.915	0.961
TGTA	76	0.967	0.126	0.014	0.938	0.996
TGTC	62	0.921	0.127	0.016	0.888	0.953
TGTG	83	0.960	0.135	0.015	0.930	0.989
TGTT	89	0.925	0.138	0.015	0.896	0.954
ATAA	103	0.974	0.109	0.011	0.952	0.995

ATAC	94	0.963	0.148	0.015	0.933	0.994
ATAG	49	1.020	0.164	0.023	0.973	1.067
ATAT	98	0.945	0.136	0.014	0.918	0.972
CTAA	30	1.005	0.077	0.014	0.976	1.033
CTAC	19	0.895	0.073	0.017	0.860	0.930
CTAG	24	0.998	0.065	0.013	0.970	1.025
CTAT	64	0.948	0.128	0.016	0.917	0.980
GTAA	93	1.001	0.127	0.013	0.974	1.027
GTAC	43	0.986	0.130	0.020	0.946	1.026
GTAG	28	1.068	0.157	0.030	1.007	1.129
GTAT	92	1.002	0.100	0.010	0.982	1.023
TTAA	103	0.925	0.111	0.011	0.904	0.947
TTAC	84	0.915	0.106	0.012	0.892	0.938
TTAG	53	1.012	0.113	0.016	0.981	1.043
TTAT	86	0.960	0.104	0.011	0.937	0.982
ATCA	104	0.967	0.165	0.016	0.935	0.999
ATCC	79	0.877	0.096	0.011	0.855	0.898
ATCG	69	0.942	0.101	0.012	0.918	0.966
ATCT	64	0.941	0.110	0.014	0.913	0.968
CTCA	95	0.892	0.109	0.011	0.870	0.914
CTCC	73	0.842	0.166	0.019	0.803	0.880
CTCG	51	0.937	0.107	0.015	0.906	0.967
CTCT	71	0.864	0.123	0.015	0.835	0.893
GTCA	70	0.983	0.129	0.015	0.952	1.014
GTCC	36	0.932	0.080	0.013	0.905	0.959
GTCG	48	0.970	0.132	0.019	0.932	1.009
GTCT	30	0.962	0.144	0.026	0.909	1.016
TTCA	81	0.917	0.115	0.013	0.891	0.942
TTCC	97	0.845	0.131	0.013	0.819	0.872
TTCG	100	0.920	0.136	0.014	0.893	0.947
TTCT	99	0.905	0.136	0.014	0.878	0.932
ATGA	85	1.017	0.105	0.011	0.994	1.039
ATGC	82	0.979	0.116	0.013	0.953	1.004
ATGG	66	1.006	0.123	0.015	0.976	1.037
ATGT	80	0.951	0.137	0.015	0.920	0.981
CTGA	89	1.008	0.141	0.015	0.979	1.038
CTGC	101	0.973	0.139	0.014	0.945	1.000
CTGG	82	1.008	0.109	0.012	0.984	1.032
CTGT	71	0.993	0.135	0.016	0.961	1.025
GTGA	86	1.026	0.125	0.013	0.999	1.053
GTGC	73	0.929	0.139	0.016	0.897	0.962
GTGG	55	1.011	0.121	0.016	0.978	1.044

GTGT	49	0.968	0.124	0.018	0.932	1.004
TTGA	97	0.983	0.125	0.013	0.957	1.008
TTGC	82	0.917	0.118	0.013	0.891	0.942
TTGG	102	0.960	0.132	0.013	0.934	0.986
TTGT	110	0.932	0.118	0.011	0.909	0.954
ATTA	107	0.908	0.105	0.010	0.887	0.928
ATTC	95	0.908	0.122	0.013	0.883	0.933
ATTG	95	1.004	0.116	0.012	0.980	1.027
ATTT	105	0.938	0.123	0.012	0.914	0.962
CTTA	48	0.910	0.108	0.016	0.879	0.941
CTTC	90	0.895	0.098	0.010	0.874	0.915
CTTG	67	0.954	0.119	0.014	0.925	0.983
CTTT	97	0.926	0.152	0.015	0.896	0.957
GTTA	81	1.041	0.145	0.016	1.009	1.073
GTTC	66	0.954	0.133	0.016	0.921	0.986
GTTG	111	0.966	0.127	0.012	0.942	0.990
GTTT	138	0.945	0.125	0.011	0.924	0.966
TTTA	93	0.937	0.117	0.012	0.913	0.961
TTTC	127	0.890	0.133	0.012	0.866	0.913
TTTG	117	0.932	0.119	0.011	0.910	0.954
TTTT	236	0.897	0.140	0.009	0.879	0.915

Designations: N – the sample size; $\overline{R}$ - mean value; S - standard deviation; $S_{\overline{R}}$ - standard error of mean.

Table S2. **The sample characteristics of relative intensities of cleavage for trinucleotides d(N_1CN_3).**

	N	$\overline{R}$	S	$S_{\overline{R}}$	The 95% confidence limits	
					Lower limit	Upper limit
ACA	263	1.133	0.192	0.012	1.110	1.157
CCA	295	1.086	0.199	0.012	1.064	1.109
GCA	359	1.239	0.232	0.012	1.215	1.263
TCA	351	1.148	0.203	0.011	1.127	1.169
ACC	274	1.010	0.134	0.008	0.994	1.026
CCC	314	0.946	0.132	0.007	0.932	0.961
GCC	277	1.091	0.164	0.010	1.072	1.110
TCC	281	0.982	0.134	0.008	0.967	0.998
ACG	296	1.441	0.329	0.019	1.403	1.479
CCG	300	1.355	0.283	0.016	1.323	1.387
GCG	361	1.568	0.440	0.023	1.523	1.614
TCG	274	1.392	0.311	0.019	1.355	1.428
ACT	245	1.102	0.190	0.012	1.078	1.126
CCT	236	1.041	0.147	0.010	1.023	1.060
GCT	330	1.256	0.219	0.012	1.232	1.279
TCT	269	1.078	0.181	0.011	1.056	1.100

Designations: N – the sample size; $\overline{R}$ - mean value; S - standard deviation; $S_{\overline{R}}$ - standard error of mean.

Mean value of each trinucleotide d(N_1CN_3) was obtained by averaging the mean values for central phosphodiester bond in tetranucleotides d($N_1CN_3N_4$) by the forth nucleotide (N_4).

Table S3. **Multiple comparison tests for population mean values of trinucleotides.**

	$\bar{R}$	Group		
CCA	1.086	1		
ACA	1.133		2	
TCA	1.148		2	
GCA	1.239			3
CCC	0.946	1		
TCC	0.982		2	
ACC	1.010		2	
GCC	1.091			3
CCG	1.355	1		
TCG	1.392	1	2	
ACG	1.441		2	
GCG	1.568			3
CCT	1.041	1		
TCT	1.078		2	
ACT	1.102		2	
GCT	1.256			3

Designations: $\bar{R}$ - mean value;

Mean value of each trinucleotide $d(N_1CN_3)$ was obtained by averaging the mean values for central phosphodiester bond in tetranucleotides $d(N_1CN_3N_4)$ by the forth nucleotide (N_4). We can state that the population means are not equal if their sample means are related to the different groups.
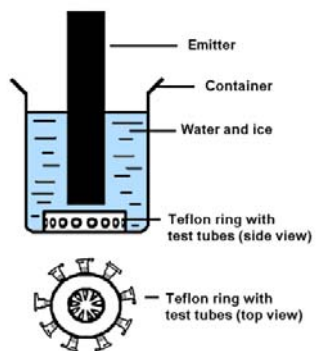
Fig. S1.